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<!--StartFragment-->RESULT 2
US-10-760-320A-4778
; Sequence 4778; Application US/10760320A
; Publication No. US20070020637A1
; GENERAL INFORMATION:
; APPLICANT: Research Association for Biotechnology
; TITLE OF INVENTION: Full length cDNA
; FILE REFERENCE: BTR-A0201Y1
; CURRENT APPLICATION NUMBER: US/10/760,320A
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: JP 2003-102206
; PRIOR FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: JP 2003-131392
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 4994
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4778
; LENGTH: 852
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-760-320A-4778

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Query Match          99.3%; Score 4392; DB 5; Length 852;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 846; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 MLITERKHFRSGRIAQSMSEANLIDMEAGKLSKSCNITECQDPDLLHNWPDFTLRGNN 60
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Db      1 MLITERKHFRSGRIAQSMSEANLIDMEAGKLSKSCNITECQDPDLLHNWPDFTLRGNN 60
      |||

Qy     61 SKVANPFWNQLSASNPFLLDDITQLRNNRKRNNISILKEDPFLFCREIENGNSFDSSGDEL 120
      |||
Db     61 SKVANPFWNQLSASNPFLLDDITQLRNNRKRNNISILKEDPFLFCREIENGNSFDSSGDEL 120
      |||

Qy    121 DVHQLLRQTSSRNSGRSKSVSELDDILDDTAHAHQSIHNSDQILLHDLWLKNDREAYKM 180
      |||
Db    121 DVHQLLRQTSSRNSGRSKSVSELDDILDDTAHAHQSIHNSDQILLHDLWLKNDREAYKM 180
      |||

Qy    181 AWLSQRQLARSCLDLNTISQSPGWAQTQLAEVTIACKVNHQGGSVQLPESDITVHVPOGH 240
      |||
Db    181 AWLSQRQLARSCLDLNTISQSPGWAQTQLAEVTIACKVNHQGGSVQLPESDITVHVPOGH 240
      |||

Qy    241 VAVGEFQEVSLRAFLDPPHMLNHDLSCTVSPLEIMLGNLNTMEALLLEMKIGAEVRKDP 300
      |||
Db    241 VAVGEFQEVSLRAFLDPPHMLNHDLSCTVSPLEIMLGNLNTMEALLLEMKIGAEVRKDP 300
      |||

Qy    301 FSQVMTEMVCLHSLGKEGPFKVLNENCYIYKDTIQVKLIDLSQVMYLVVAAQAKALPSPAA 360
      |||
Db    301 FSQVMTEMVCLHSLGKEGPFKVLNENCYIYKDTIQVKLIDLSQVMYLVVAAQAKALPSPAA 360
      |||

Qy    361 TIWDYIHKTTSIGIYGPKYIHPNFTTVVLTVCGHNYMPGQLTISDIKKGGKKNISPVVFQLW 420
      |||
Db    361 TIWDYIHKTTSIGIYGPKYIHPNFTTVVLTVCGHNYMPGQLTISDIKKGGKKNISPVVFQLW 420
      |||

Qy    421 GKQSFLLDKPDLSISIFSCDPDFEVKTEGERKEIKQKQLEAGEVVHQQLFSLVEHREM 480
      |||
Db    421 GKQSFLLDKPDLSISIFSCDPDFEVKTEGERKEIKQKQLEAGEVVHQQLFSLVEHREM 480
      |||

Qy    481 HLFDFCVQVEPPNGEPVAQFSITTPDPTPNLKRLLNPGYLQKKEEIKSAPLSPKILVKY 540
      |||
Db    481 HLFDFCVQVEPPNGEPVAQFSITTPDPTPNLKRLLNPGYLQKKEEIKSAPLSPKILVKY 540
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Qy    541 PTFQDKTLNFSNYGVTLKAVLRQSKIDYFLEYFKGDTIALLGEGKVKAIQSKVKKEWYVG 600
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Db    541 PTFQDKTLNFSNYGVTLKAVLRQSKIDYFLEYFKGDTIALLGEGKVKAIQSKVKKEWYVG 600
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Qy      601 VLRGKIGLVHCKNVKVISKEQVMFMSDSVFTTRNLLEQIVLPLKKLTYIYSVVLTLVSEK 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 VLRGKIGLVHCKNVKVISKEQVMFMSDSVFTTRNLLEQIVLPLKKLTYIYSVVLTLVSEK 660

Qy      661 VYDWKVLADV LGYSHLSLEDFDQIQADKESEKVS YVIKKLKEDCHTERNTRKFLYELIVA 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 VYDWKVLADV LGYSHLSLEDFDQIQADKESEKVS YVIKKLKEDCHTERNTRKFLYELIVA 720

Qy      721 LLKMDCQELVARLIQEAAVLTSAVKLGKGWRELAEKLVRLTKQQMEAYEIPHRGNTGDVA 780
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 LLKMDCQELVARLIQEAAVLTSAVKLGKGWRELAEKLVRLTKQQMEAYEIPHRGNTGDVA 780

Qy      781 VEMMWKPAYDFLYTWSAHYGNNYRDVLQDLQSALDRMKNPVTKHWRELTGVLILVNSLEV 840
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 VEMMWKPAYDFLYTWSAHYGNNYTDVLQDLQSALDRMKNPVTKHWRELTGVLILVNSLEV 840

Qy      841 LRVTAFASTSEEV 852
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Db      841 LRVTAFASTSEEV 852

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&lt;!--StartFragment--&gt;RESULT 3

US-10-760-320A-4471

; Sequence 4471, Application US/10760320A

; Publication No. US20070020637A1

; GENERAL INFORMATION:

; APPLICANT: Research Association for Biotechnology

; TITLE OF INVENTION: Full length cDNA

; FILE REFERENCE: BTR-A0201Y1

; CURRENT APPLICATION NUMBER: US/10/760,320A

; CURRENT FILING DATE: 2004-01-21

; PRIOR APPLICATION NUMBER: JP 2003-102206

; PRIOR FILING DATE: 2003-01-21

; PRIOR APPLICATION NUMBER: JP 2003-131392

; PRIOR FILING DATE: 2003-05-09

; NUMBER OF SEQ ID NOS: 4994

; SOFTWARE: PatentIn Ver. 3.1

; SEQ ID NO 4471

; LENGTH: 3188

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-760-320A-4471

Query Match 99.6%; Score 2547.8; DB 14; Length 3188;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2552; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ATGCTAATCACTGAAAGAAAACATTTTCGGTCAGGAAGAATTGCACAAAGTATGTCTGAA 60  
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Db 310 ATGCTAATCACTGAAAGAAAACATTTTCGGTCAGGAAGAATTGCACAAAGTATGTCTGAA 369  
| | | | |  
Qy 61 GCAAATTTGATTGACATGGAAGCTGGAAAAGTCTCAAAAAGTTGCAATATTACAGAATGC 120  
| | | | |  
Db 370 GCAAATTTGATTGACATGGAAGCTGGAAAAGTCTCAAAAAGTTGCAATATTACAGAATGC 429  
| | | | |  
Qy 121 CAGGACCCAGACTTGCTTCACAATTGGCCGGATGCTTTCACCCTTCGTGGTAATAATGCT 180  
| | | | |  
Db 430 CAGGACCCAGACTTGCTTCACAATTGGCCGGATGCTTTCACCCTTCGTGGTAATAATGCT 489  
| | | | |  
Qy 181 TCCAAAGTTGCAAATCCATTCTGGAATCAACTGTCTGCTTCTAACCATTCTTTGGATGAC 240  
| | | | |  
Db 490 TCCAAAGTTGCAAATCCATTCTGGAATCAACTGTCTGCTTCTAACCATTCTTTGGATGAC 549  
| | | | |  
Qy 241 ATAACCTCAACTAAGAAATAACAGGAAGAGAAATAATATTTCCATCTTAAAGGAAGATCCT 300  
| | | | |  
Db 550 ATAACCTCAACTAAGAAATAACAGGAAGAGAAATAATATTTCCATCTTAAAGGAAGATCCT 609  
| | | | |  
Qy 301 TTTCTTTTCTGTAGAGAAATAGAAAATGGAAATCTTTTGATTCTCCGGTGATGAACTT 360  
| | | | |  
Db 610 TTTCTTTTCTGTAGAGAAATAGAAAATGGAAATCTTTTGATTCTCCGGTGATGAACTT 669  
| | | | |  
Qy 361 GATGTGCATCAGTTACTTAGGCAGACTTCCTCAAGAAATCTGGAAGATCTAAAAGTGTT 420  
| | | | |  
Db 670 GATGTGCATCAGTTACTTAGGCAGACTTCCTCAAGAAATCTGGAAGATCTAAAAGTGTT 729  
| | | | |  
Qy 421 TCAGAACTTCTGGACATTTTAGACGACACAGCACATGCCCATCAGAGTATACATAACTCT 480  
| | | | |  
Db 730 TCAGAACTTCTGGACATTTTAGACGACACAGCACATGCCCATCAGAGTATACATAACTCT 789  
| | | | |  
Qy 481 GACCAGATCCTACTACACGACTTAGAGTGGCTTAAAAATGATCGGGAGGCTTATAAAATG 540  
| | | | |  
Db 790 GACCAGATCCTACTACACGACTTAGAGTGGCTTAAAAATGATCGGGAGGCTTATAAAATG 849  
| | | | |  
Qy 541 GCTTGGTTAAGTCAACGCCAGCTGGCCCCGCTCCTGCCTTGATTGAATACAATTAGTCAG 600  
| | | | |  
Db 850 GCTTGGTTAAGTCAACGCCAGCTGGCCCCGCTCCTGCCTTGATTGAATACAATTAGTCAG 909  
| | | | |

Qy	601	AGCCCTGGATGGGCCAGACACAACCTTGCGGAGGTCACCATAGCTTGCAAAGTAAACCAT	660
Db	910	AGCCCTGGATGGGCCAGACACAACCTTGCGGAGGTCACCATAGCTTGCAAAGTAAACCAT	969
Qy	661	CAAGGAGGGTCAGTACAATTACCTGAATCAGACATCACTGTTTCATGTGCCCCAAGGTCAT	720
Db	970	CAAGGAGGGTCAGTACAATTACCTGAATCAGACATCACTGTTTCATGTGCCCCAAGGTCAT	1029
Qy	721	GTGGCTGTGGGAGAATTCCAAGAGGTGTCTCTAAGGGCTTTCCTTGATCCGCCACACATG	780
Db	1030	GTGGCTGTGGGAGAATTCCAAGAGGTGTCTCTAAGGGCTTTCCTTGATCCGCCACACATG	1089
Qy	781	CTTAACCATGATCTTTCGTGCACTGTGAGCCCGTTGTTGGAAATCATGTTAGGCAACCTC	840
Db	1090	CTTAACCATGATCTTTCGTGCACTGTGAGCCCGTTGTTGGAAATCATGTTAGGCAACCTC	1149
Qy	841	AATACAATGGAAGCCCTTTTGCTGGAGATGAAAATTGGGGCTGAAGTAAGAAAGGATCCT	900
Db	1150	AATACAATGGAAGCCCTTTTGCTGGAGATGAAAATTGGGGCTGAAGTAAGAAAGGATCCT	1209
Qy	901	TTCAGCCAAGTCATGACAGAAATGGTGTGTTTACACAGCTTGGGTAAAGAAGGCCCTTTT	960
Db	1210	TTCAGCCAAGTCATGACAGAAATGGTGTGTTTACACAGCTTGGGTAAAGAAGGCCCTTTT	1269
Qy	961	AAAGTTTTAAAGCAACTGCTACATTTATAAAGACACCATCCAAGTCAAGCTAATCGACTTG	1020
Db	1270	AAAGTTTTAAAGCAACTGCTACATTTATAAAGACACCATCCAAGTCAAGCTAATCGACTTG	1329
Qy	1021	AGTCAGGTAATGTATCTAGTGGTTGCTGCACAAGCTAAAGCTCTTCCGTCACCAGCTGCC	1080
Db	1330	AGTCAGGTAATGTATCTAGTGGTTGCTGCACAAGCTAAAGCTCTTCCGTCACCAGCTGCC	1389
Qy	1081	ACCATTTGGGATTATATCCACAAAACCACCTCAATTGGAATTTATGGACCCAAATATATC	1140
Db	1390	ACCATTTGGGATTATATCCACAAAACCACCTCAATTGGAATTTATGGACCCAAATATATC	1449
Qy	1141	CATCCCAGTTTACTGTTGTTTTAACAGTTTGTGGACACAATTATATGCCAGGACAGCTT	1200
Db	1450	CATCCCAGTTTACTGTTGTTTTAACAGTTTGTGGACACAATTATATGCCAGGACAGCTT	1509
Qy	1201	ACAATTTCTGATATTAAGAAGGGTGGAAAAACATATCTCCAGTTGTGTTTCAGCTCTGG	1260
Db	1510	ACAATTTCTGATATTAAGAAGGGTGGAAAAACATATCTCCAGTTGTGTTTCAGCTCTGG	1569
Qy	1261	GGGAAGCAGTCATTTTTACTTGACAAGCCACAAGATTTAAGTATTTCTATTTTTCTCTGT	1320
Db	1570	GGGAAGCAGTCATTTTTACTTGACAAGCCACAAGATTTAAGTATTTCTATTTTTCTCTGT	1629
Qy	1321	GATCCTGATTTTGAAGTAAAGACAGAAGGAGAAAGGAAAGAAATTAAACAAAAGCAGTTG	1380
Db	1630	GATCCTGATTTTGAAGTAAAGACAGAAGGAGAAAGGAAAGAAATTAAACAAAAGCAGTTG	1689
Qy	1381	GAAGCAGGTGAAGTAGTTCATCAACAATTTTATTTTCTTTAGTTGAGCACAGAGAGATG	1440
Db	1690	GAAGCAGGTGAAGTAGTTCATCAACAATTTTATTTTCTTTAGTTGAGCACAGAGAGATG	1749
Qy	1441	CAC TTGTTTGATTTTTGTGTTCAAGTGGAGCCTCCCAATGGTGAACCAGTTGCACAGTTC	1500
Db	1750	CAC TTGTTTGATTTTTGTGTTCAAGTGGAGCCTCCCAATGGTGAACCAGTTGCACAGTTC	1809
Qy	1501	TCTATCACTACTCCTGATCCAACCCCAAACCTAAAAAGACTCTCGAATCTGCCAGGCTAT	1560
Db	1810	TCTATCACTACTCCTGATCCAACCCCAAACCTAAAAAGACTCTTGAATCTGCCAGGCTAT	1869

Qy	1561	TTGCAGAAGAAGGAGGAAATCAAGTCTGCTCCTTTATCACCAAAAATTCCTTGTTAAATAT	1620
Db	1870	TTGCAGAAGAAGGAGGAAATCAAGTCTGCTCCTTTATCACCAAAAATTCCTTGTTAAATAT	1929
Qy	1621	CCTACATTTCAAGATAAAACATTGAACTTTAGCAACTATGGGGTAACCCTGAAGGCAGTG	1680
Db	1930	CCTACATTTCAAGATAAAACATTGAACTTTAGCAACTATGGGGTAACCCTGAAGGCAGTG	1989
Qy	1681	CTAAGACAAAGCAAGATTGATTACTTCCTTGAATATTTCAAAGGGGACACAATAGCTCTC	1740
Db	1990	CTAAGACAAAGCAAGATTGATTACTTCCTTGAATATTTCAAAGGGGACACAATAGCTCTC	2049
Qy	1741	CTCGGGGAAGGTAAGGTAAAAGCTATTGGTCAGTCCAAAGTGAAAGAATGGTATGTAGGA	1800
Db	2050	CTCGGGGAAGGTAAGGTAAAAGCTATTGGTCAGTCCAAAGTGAAAGAATGGTATGTAGGA	2109
Qy	1801	GTCCTCAGAGGTAAGATTGGACTTGTACACTGCAAAAATGTCAAGGTGATTTCAAAGGAG	1860
Db	2110	GTCCTCAGAGGTAAGATTGGACTTGTACACTGCAAAAATGTCAAGGTGATTTCAAAGGAG	2169
Qy	1861	CAAGTAATGTTTATGTCAGATAGTGTCTTTACAACCAGAAATCTTCTTGAACAGATTGTC	1920
Db	2170	CAAGTAATGTTTATGTCAGATAGTGTCTTTACAACCAGAAATCTTCTTGAACAGATTGTC	2229
Qy	1921	CTGCCCTTTAAAAAAATTGACTTATATCTACTCAGTTGTATTAACCTTGGTGTGAGAAAA	1980
Db	2230	CTGCCCTTTAAAAAAATTGACTTATATCTACTCAGTTGTATTAACCTTGGTGTGAGAAAA	2289
Qy	1981	GTTTATGATTGGAAAGTTTGTAGCTGATGTCCTGGGTACTCACATCTGTCCCTGGAAGAT	2040
Db	2290	GTTTATGATTGGAAAGTTTGTAGCTGATGTCCTGGGTACTCACATCTGTCCCTGGAAGAT	2349
Qy	2041	TTTGATCAAATTCAGCAGACAAAGAATCAGAGAAAGTTTCTTATGTTATAAAGAAGTTA	2100
Db	2350	TTTGATCAAATTCAGCAGACAAAGAATCAGAGAAAGTTTCTTATGTTATAAAGAAGTTA	2409
Qy	2101	AAGGAAGATTGCCACACAGAGAGAAATACAAGGAAGTTTCTGTATGAACTTATTGTGGCT	2160
Db	2410	AAGGAAGATTGCCACACAGAGAGAAATACAAGGAAGTTTCTGTATGAACTTATTGTGGCT	2469
Qy	2161	CTTCTGAAAATGGATTGCCAAGAGTTAGTCGCACGTCTCATCCAAGAAGCTGCTGTTCTG	2220
Db	2470	CTTCTGAAAATGGATTGCCAAGAGTTAGTCGCACGTCTCATCCAAGAAGCTGCTGTTCTG	2529
Qy	2221	ACTTCAGCTGTCAAGCTTGGAAAAGGCTGGAGGGAAGTAGCTGAAAAGTTAGTACGACTC	2280
Db	2530	ACTTCAGCTGTCAAGCTTGGAAAAGGCTGGAGGGAAGTAGCTGAAAAGTTAGTACGACTC	2589
Qy	2281	ACAAAGCAACAAATGGAGGCATATGAAATTCCTCATCGAGGAAACACTGGAGATGTTGCT	2340
Db	2590	ACAAAGCAACAAATGGAGGCATATGAAATTCCTCATCGAGGAAACACTGGAGATGTTGCT	2649
Qy	2341	GTTGAGATGATGTGGAACCTGCCTATGATTTTCTGTATACCTGGAGTGCTCACTATGGA	2400
Db	2650	GTTGAGATGATGTGGAACCTGCCTATGATTTTCTGTATACCTGGAGTGCTCACTATGGA	2709
Qy	2401	AATAACTACAGAGATGTGTTACAAGACCTTCAGTCAGCTTTGGACAGAATGAAAAACCTT	2460
Db	2710	AATAACTACAGAGATGTGTTACAAGACCTTCAGTCAGCTTTGGACAGAATGAAAAACCTT	2769
Qy	2461	GTGACTAAACACTGGAGAGAAATTAAGTGGAGTTTTAATACTAGTAAATTCCTTGGAGGTT	2520
Db	2770	GTGACTAAACACTGGAGAGAAATTAAGTGGAGTTTTAATACTAGTAAATTCCTTGGAGGTT	2829
Qy	2521	TTGAGAGTAACTGCATTCTCCACTTCTGAGGAAGTATAG	2559

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Db 2830 TTGAGAGTAACTGCATTCTCCACTTCTGAGGAAGTATAG 2868

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